

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: February 16, 2005, 16:12:05 ; Search time 168.877 Seconds  
(without alignments)  
2810.909 Million cell updates/sec

Title: US-10-003-356-8  
Perfect score: 4904  
Sequence: 1 MFERRKEQDEGPGIHEFLAF.....TVSTVLDRVLTYMCPLKIQ 927

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt\_03.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3962	80.8	912	2	O70410
2	2980	60.8	755	2	O8NGV9
3	2296.5	46.8	618	2	O8C0V4
4	1749	35.7	365	2	O8TDU1
5	1727	35.2	428	2	O70413
6	1695.5	34.6	1085	1	CASR_BOVIN
7	1693.5	34.5	476	2	O8C0M6
8	1691.5	34.5	1079	2	O80ZAB
9	1690.5	34.5	1079	1	CASR_RAT
10	1688.5	34.4	1027	2	O8J104
11	1687.5	34.4	1078	1	CASR_HUMAN
12	1685.5	34.4	1079	1	CASR_MOUSE
13	1630.5	33.2	940	2	O90WL6
14	1630.5	33.2	941	2	O6XAF1
15	1629.5	33.2	941	2	O6XAF3
16	1614	32.9	940	2	O73635
17	1609.5	32.8	880	2	O73639
18	1594.5	32.5	850	2	O6XAF2
19	1551.5	31.6	848	2	O93553
20	1529	31.2	856	2	O73638
21	1497	30.5	864	2	O73637
22	1437	29.3	868	2	O73636
23	1417.5	28.9	854	2	O6UNX3
24	1390	28.3	844	2	O93552
25	1332.5	27.2	875	2	O73640
26	1108.5	22.6	783	2	O8CDP3
27	1074	21.9	855	2	O70409
28	1071	21.8	928	2	O8K4Z6
29	1066	21.7	928	2	O70VB1
30	1063	21.7	926	2	O8NH29
31	1062	21.7	855	2	O6TAC4

32	1017	20.7	879	2	O8NGU8	Q8NGU8 homo sapien
33	990	20.2	877	2	O9PW88	Q9PW88 carassius a
34	974.5	19.9	855	2	O6JK43	O6JK43 homo sapien
35	964	19.7	865	2	O80Z09	O80Z09 mus musculus
36	961	19.6	779	2	O35269	O35269 rattus norv
37	955	19.5	842	2	O99PG5	O99PG5 mus musculus
38	950	19.4	842	2	O92515	O92515 mus musculus
39	943	19.2	842	2	O923J9	O923J9 mus musculus
40	942	19.2	840	2	O920R8	O920R8 rattus norv
41	940.5	19.2	888	2	O767K3	O767K3 xenopus lae
42	939	19.1	842	2	O99PG6	O99PG6 mus musculus
43	912	18.6	866	2	O35268	O35268 rattus norv
44	904.5	18.4	230	2	O70414	O70414 rattus norv
45	901.5	18.4	751	2	O6JK44	O6JK44 homo sapien

#### ALIGNMENTS

##### RESULT 1

O70410 PRELIMINARY; PRT; 912 AA.  
AC O70410;  
DT 01-AUG-1998 (TrEMBLrel. 07, Created)  
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Putative pheromone receptor V2R2.  
OS Mus musculus (Mouse)  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Vomeranosal neurons;  
RX MEDLINE=97436753; PubMed=9292726; DOI=10.1016/S0896-6273(00)80946-0;  
RA Ryba N.J., Tirindelli R.;  
RT "A new multigene family of putative pheromone receptors."  
RL Neuron 19:371-379(1997).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Vomeranosal neurons;  
RA Ryba N.J., Tirindelli R.;  
RL SUBMITTED (MAR-1998) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF053986; AAC08413.1; -  
DR HSSP; P23385; LEWK  
DR GO; GO:0016020; C:membrane; IEA.  
DR GO; GO:0008067; F:metabotropic glutamate, GABA-B-like recepto...; IEA.  
DR GO; GO:0004872; F:receptor activity; IEA.  
DR InterPro; IPR001828; ANF receptor.  
DR InterPro; IPR000068; Ca\_sens receptor.  
DR InterPro; IPR000337; GPCR\_MgR.  
DR InterPro; IPR011500; NCD3G\_GPCR.  
DR Pfam; PF00003; 7tm 3; 1.  
DR Pfam; PF01094; ANF receptor; 1.  
DR Pfam; PF07562; NCD3G; 1.  
DR PRINTS; PR00592; CASSENSINGR.  
DR PRINTS; PR00248; GPCR\_MGR.  
DR PROSITE; PS00259; G\_PROTEIN\_RECEP\_F3\_4; 1.  
KW Receptor.  
SQ SEQUENCE 912 AA; 102348 MW; 2C54FAB6DFBFA48D CRC64;

Query Match. 80.8%; Score 3962; DB 2; Length 912;

Best Local Similarity 82.6%; Pred. No. 28-270;

Matches 747; Conservative 62; Mismatches 87; Indels 8; Gaps 2;

QY 17 FLAFLWAEIGSBAKEEKEERTCLGK-----CYDAENHSLVIGLFFIDRTIPANES 71

Db 12 FLAFLWAVLGA---QNKTEEVQCLMAKFNLSGYVDKKNHSLVIGLFFIHSRIIPVDEA 68

QY 72 ILEPASACEGNGFORFRMKAMIMIKKINRKOILPNITLGYQIFDTCFTISKSVEAV 131

Db 69 ILEVPSPMCEGNGFRFRMKMTIHTKEINERKDIPLNHTLGYQIFDSCYTISKAMBS 128

QY 132 LVFLTGQENRPNFRNPGAGIVGAGSFLSPASRIILGLYLPOVGTSTCVILSD 191  
 Db 129 LVFLTGQEFNFRNPGSTLAALVSGSGSLVAASRIILGLYMPQVGTSSCSILSD 188  
 QY 192 KYPPSYLRVLIASDKIQSKAVVYKRIQHFGVWVWGAIAADDDYGYGYVKTKEKMSANLC 251  
 Db 189 KPFPYSYLRVLPNDNLQSEAVNLIKHFGVWVWGAIAADDDYGYGYVKTKEKMSANLC 248  
 QY 252 VAFSTIPKVSNEKQKAVKAVTSTAKVILVITSDILSLFVLEMHNIIDRTWIAT 311  
 Db 249 VAFSTIPKVSNEKQKAVKAVTSTAKVILVITSDILSLFVLEMHNIIDRTWIAT 308  
 QY 312 EAMITSALIAKPEYPPYGGTIGFATPSRVIPLGKFLYDVHPNKDNDVLTTFEWTAF 371  
 Db 309 EAMITSALIAKPEYPPYGGTIGFATPSRVIPLGKFLYDVHPNKDNDVLTTFEWTAF 368  
 QY 372 NCTWPNSSVPYVHRVNMVKEDRLYDMSDQLCTGEEKLEDKNTYLDTSQLRITKQCK 431  
 Db 369 NCTWPNSSVPYVHRVNMVKEDRLYDMSDQLCTGEEKLEDKNTYLDTSQLRITKQCK 428  
 QY 432 QAVYAIAGHLHLSRQCGQPGSNOQCAIYPTDFWQMLMYMKEIKFKSHEDKWILD 491  
 Db 429 QAVYAIAGHLHLSRQCGQPGSNOQCAIYPTDFWQMLMYMKEIKFKSHEDKWILD 488  
 QY 492 DNGDLKNGHYDVLANWHLDDGEISFVTVGRNFRSTNPFELVPTNSTIFWNTSSRLPHS 551  
 Db 489 DNGDLKNGHYDVLANWHLDDGEISFVTVGRNFRSTNPFELVPTNSTIFWNTSSRLPHS 548  
 QY 552 VCTDVCPPGTGRGVFQREPICCFDSIPCADGHVSRKPGERECEQCGDYMSNAQKSECVL 611  
 Db 549 FCTQVCPGTRKIRQGOPICCFDCIPCADGVSEKSGQRECDPCGEDDSNAGSKCVP 608  
 QY 612 KEVEYLAIDBALGFTLVLSVFGAFVLAIVATVVIHRHTPLVNASDQGLFIQVSLII 671  
 Db 609 KLVEYLAIDBALGFTLVLSVFGAFVLAIVATVVIHRHTPLVNASDQGLFIQVSLII 668  
 QY 672 MLSSMLFIDKPHNWSMAGOVTLALGFLCLCLGKTSLSFLAYRISKSTQLSMHP 731  
 Db 669 TVLSLLFIHGPNWSCWARGITLALGFLCLCLGKTSLSFLAYRISKSTQLSMHP 728  
 QY 732 LYRKIVLISVLAIGICTAYLILEPPMVKNMSQNTKIILGCNEISIFLYSMFGIDA 791  
 Db 729 IPRKIVLVVGVGEIGVCAAVLLEPPMPKNIQVKKIIFECNEGSVEFLCSIFGQV 788  
 QY 792 FLALICFTTVAQRLPNYEGCITFGMLVFFIWMSPVVLSTKGFPAVEIFAI 851  
 Db 789 LRALICFTTVAQRLPNYEGCITFGMLVFFIWMSPVVLSTKGFPAVEIFAI 848  
 QY 852 LASSHLLGCFAPAKCLILLRPNRTSEIVCGRVSTTDNCIOLTSAPVSELNNTTST 911  
 Db 849 LASSHLLGCFAPAKCLILLRPNRTSEIVCGRVSTTDNCIOLTSAPVSELNNTTST 908  
 QY 912 VLDD 915  
 Db 909 VLDE 912

## RESULT 2

Q8NGV9 ID Q8NGV9 PRELIMINARY; PRT; 755 AA.  
 AC Q8NGV9;  
 DT 01-OCT-2002 (TremBLrel. 22, Created)  
 DT 01-OCT-2002 (TremBLrel. 22, Last sequence update)  
 DT 01-JUN-2003 (TremBLrel. 24, Last annotation update)  
 DE Seven transmembrane helix receptor.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxId=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Suwa M., Sato T., Okouchi I., Arita M., Futami K., Matsumoto S.,  
 RA Tautsuni S., Aburatani H., Asai K., Akiyama Y.;

RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AB065664; BAC03890.1; -.  
 DR GO; GO:0016021; C:integral to membrane; IEA.  
 DR GO; GO:0008067; F:metabotropic glutamate, GABA-B-like recepto. .; IEA.  
 DR GO; GO:0004872; F:receptor activity; IEA.  
 DR InterPro; IPR001828; ANF\_receptor.  
 DR InterPro; IPR000337; GPCR\_Mgr.  
 DR Pfam; PF00003; 7tm\_3; 1.  
 DR Pfam; PF01094; ANF\_receptor; 1.  
 DR PRINTS; PR00248; GPCRMR.  
 DR PROSITE; PS00259; G\_PROTEIN\_RECPEP\_F3\_4; 1.  
 KW Receptor; Transmembrane.  
 SQ SEQUENCE 755 AA; 83791 MW; 04D56AD8917BDA1F CRC64;

Query Match 60.8%; Score 2980; DB 2; Length 755;  
 Best Local Similarity 66.1%; Pred. No. 2.7e-201;  
 Matches 621; Conservative 34; Mismatches 88; Indels 196; Gaps 13;  
 QY 1 MPERRKEQDEGPGIHEFLAFLWAEIGSEAKEBEERTCRLLGKCVDAENHSLVIGLFP 60  
 Db 1 MPERRKEQDEGPGIHEFLAFLWAEIGSEAKEBEERTCRLLGKCVDAENHSLVIGLFP 60  
 QY 61 IDSRTIPANESILEPASAKCEGFNFRWMMKAMIMKEINKRKDILPNITLGYQIFDT 120  
 Db 61 IDSRTIPANESILEPASAKCEGFNFRWMMKAMIMKEINKRKDILPNITLGYQIFDT 120  
 QY 121 CFTTISKVAVLVLTGQENRPNFRNPGAGIVGAGSFLSPASRIILGLYLPOV 180  
 Db 121 CFTTISKVAVLVLTGQENRPNFRNPGAGIVGAGSFLSPASRIILGLYLPOV 180  
 QY 181 GYTSTCVILSDKYQFYSYLRVLTASDKIQSKAVVYKRIQHFGVWVWGAIAADDDYGYGYVKT 240  
 Db 181 GYTSTCVILSDKYQFYSYLRVLTASDKIQSKAVVYKRIQHFGVWVWGAIAADDDYGYGYVKT 223  
 QY 241 FKEKESANLCVAFSTIPKVSNEKQKAVKAVTSTAKVILVITSDILSLFVLEMH 300  
 Db 241 LSPRLSCSGAILA-----TG-----FCHVAQAGLEFLASNYL 237  
 QY 301 HNTDRTIATEAMITSAIAKPEYPPYGGTIGFATPSRVIPLGKFLYDVHPNKDND 360  
 Db 238 GNL-----TG-----FCHVAQAGLEFLASNYL 240  
 QY 361 VLTIEFWQTAFTNCTWPNSSVPYVHRVNMVKEDRLYDMSDQLCTGEEKLEDKNTYL 419  
 Db 241 CLPVE-----TG-----FCHVAQAGLEFLASNYL 264  
 QY 420 DTSQLRITKQCKQAVYAIAGHLHLSRQCGQPGSNOQCAIYPTDFWQML---MYMK 476  
 Db 265 TASASQ-----SAGITGVSH-----CAMPSTIELMIQHIYFRM 299  
 QY 477 EIKFKSHEDKWILDNDGDLKNGHYDVLANWHLDDGEISFV---TVGRNFRSTNPFELV 534  
 Db 300 NCRVTTESRSVAMLEYSGEISAHCHLCLLGSSNSPASAPLVAGTGAHHAQLIFVFLVE 359  
 QY 535 TNSTIEFWNTSSRLPHSV-----CTDVCVCP---PGTGRGVFQREPICCFDSIPCADGHVSRKP 588  
 Db 360 TG---FHHVSDQGLDLSISFPITQCLVCLVGLGRGVFQREPICCFDSIPCADGHVSRKP 416  
 QY 589 GERECQCGEDYWSNAQKSECVLKEVEYLAIDBALGFTLVLSVFGAFVLAIVATVVIH 648  
 Db 417 GERECQCGEDYWSNAQKSECVLKEVEYLAIDBALGFTLVLSVFGAFVLAIVATVVIH 476  
 QY 649 RHTPLVNASDQGLFIQVSLIIMLLSMLFIDKPHNWSMAGOVTLALGFLSLCLSLG 708  
 Db 477 RHTPLVNASDQGLFIQVSLIIMLLSMLFIDKPHNWSMAGOVTLALGFLSLCLSLG 536  
 QY 709 KTSLSFLAYRISKSTQLSMHPYKRIIVLSVLAIEIGICTAYLILEPPMVKNMSQNT 768  
 Db 537 KTSLSFLAYRISKSTQLSMHPYKRIIVLSVLAIEIGICTAYLILEPPMVKNMSQNT 596  
 QY 769 TKIILGCNEISIFLYSMFGIDAFLALCLFTTVAQRLPNYEGCITFGMLVFFIWM 828  
 Db 597 TKIILGCNEISIFLYSMFGIDAFLALCLFTTVAQRLPNYEGCITFGMLVFFIWM 656

QY 829 MSFVYVLTGKFKMAVEIFAILASSHGLGCIAPKCLIIILLRPRNTSEIVCGRVST 988  
 DB 657 MSFVYVLTGKFKMAVEIFAILASSHGLGCIAPKCLIIILLRPRNTSEIVCGRVST 716  
 QY 889 TDNCIQLTSAFVSSELNNTTVSTVLDRLVLYNCPLKQ 927  
 DB 717 TDNCIQLTSAFVSSELNNTTVSTVLDRLVLYNCPLKQ 755

RESULT 3  
 Q8C0V4 PRELIMINARY; PRT; 618 AA.  
 AC Q8C0V4;  
 DT 01-MAR-2003 (TREMUREl. 23, Created)  
 DT 01-MAR-2003 (TREMUREl. 23, Last sequence update)  
 DT 01-JUN-2003 (TREMUREl. 24, Last annotation update)  
 DE Mus musculus adult male testis cDNA, RIKEN full-length enriched  
 DE library, clone:4930518C23 product:weakly similar to PUTATIVE PHEROMONE  
 DE RECEPTOR V2R2, full insert sequence.  
 GN Name=4930518C23Rik;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OC NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Testis;  
 RX MEDLINE=9279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;  
 RA Carninci P., Hayashizaki Y.;  
 RT "High-efficiency full-length cDNA cloning.";  
 RL Meth. Enzymol. 303:19-44(1999).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Testis;  
 RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;  
 RA RIKEN FANTOM Consortium;  
 RT "Functional annotation of a full-length mouse cDNA collection.";  
 RL Nature 409:685-690(2001).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Testis;  
 RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;  
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,  
 RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;  
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to  
 RT prepare full-length cDNA libraries for rapid discovery of new genes.";  
 RL Nature Res. 10:1617-1630(2000).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Testis;  
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;  
 RA Shibata K., Itoh M., Aizawa K., Nagao S., Sasaki N., Carninci P.,  
 RA Konno H., Akiyama J., Nishi K., Kitanai T., Tashiro H., Itoh M.,  
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,  
 RA Yamamoto K., Matsunoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,  
 RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,  
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,  
 RA Okazaki Y., Muramatsu M., Inoue Y., Kita A., Hayashizaki Y.;  
 RT "RIKEN integrated sequence analysis (RISA) system-384-format  
 RT sequencing pipeline with 384 multicapillary sequencer.";  
 RL Genome Res. 10:1757-1771(2000).  
 RN [6]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Testis;

RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,  
 RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,  
 RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,  
 RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,  
 RA Kato H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,  
 RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,  
 RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,  
 RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,  
 RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,  
 RA Tagawa A., Takahashi F., Takaku-Akaira S., Takeda Y., Tanaka T.,  
 RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.,  
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AK029734; BAC26588.1; -;  
 DR MGD; MGI:2441682; 4930518C23Rik.  
 DR GO; GO:0016021; C:integral to membrane; TAS.  
 DR GO; GO:0004930; P:G-protein coupled receptor activity; TAS.  
 DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; TAS.  
 DR InterPro; IPR001828; ANF\_receptor.  
 DR InterPro; IPR000068; Ca\_sens\_receptor.  
 DR InterPro; IPR000337; GPCR\_Mgr.  
 DR InterPro; IPR011500; NCD3G\_GPCR.  
 DR Pfam; PF01094; ANF\_receptor; 1.  
 DR Pfam; PF07562; NCD3G; 1.  
 DR PRINTS; PR00592; CASENSINGR.  
 DR PRINTS; PR00248; GPCRMRGR.  
 KW Receptor.  
 SQ SEQUENCE 618 AA; 69142 MW; 240B395BACCD5424 CRC64;  
 Query Match 46.8%; Score 2296.5; DB 2; Length 618;  
 Best Local Similarity 72.7%; Pred. No. 3.3e-153;  
 Matches 424; Conservative 73; Mismatches 81; Indels 5; Gaps 2;  
 QY 64 RTIPANESILBPASAKCEGFNFRFRMKAMTHMKRDKILPNITLGVIQIDTCFT 123  
 DB 19 RIMPISDDEIEIESPMCEGFNFRGRMKMTLHTKEINERKDIILPNHTLGVIQIDTCFS 78  
 QY 124 ISKSEAVLVLFTGQENRPNRSTGAPGIVGAGGSFLSVASRILGLYLPQVGT 183  
 DB 79 VSKAMETAMTLTGQEEKPNRSTGKYLVIIGSGSSLSVTAARIFGLYMPQVGT 138  
 QY 184 STCVILSDKYOPPSVLRVIASDKIOSKAVKRIQHFGVWVWCAIAADDDYGVKVTPE 243  
 DB 139 SSSAILSDKFPQSPFIRSIPSKIQIEAMVTLLIHFVWVWGAIASEDDYGVKVSFRE 198  
 QY 244 KMSANLVCAPSETIPKVSNEKMKAVKAVKSTAKVILVTSIDILSLFVLEIHHNI 303  
 DB 199 KMETANLVCAPSETIPKVSNERMQKAVKAKSSAKVILVTSIDILSPFVLEVIHNI 258  
 QY 304 TDRTWIATEAWITSALIAKPEYFPYFGTIGPATPRSVIPGLKEFLYDVHPKDPNDVLT 363  
 DB 259 THTTWIASEAWITSALIAKPEYFPYFGTIGPATPRSVIPGLKEFLYDVHPKDPNDVLT 318  
 QY 364 IEFWQTAFTNCTWPNSSVPYNDHRVNMVTKEDRLYDMSDOLCTGKEKLEDKNTYLDTSQ 423  
 DB 319 IEFWQTAFTNCTWPNSSVPYNDHRVNMVTKEDRLYDMSDOLCTGKEKLEDKNTYLDTSQ 378  
 QY 424 LRITKQCKQAVYIAHGLDLHLSRCQ--EGQGFPGNSQOCAYIPTDFWQLMYMYKEIKFK 481  
 DB 379 LRITNNVQAVYIMAHLDHLSTCDLLEEQ---RNTACSHIPDFEPKELLFPFKLKIT 435  
 QY 482 SHEDKWIILDDNGLKNGHYDVNLNHLDDDEGISFVTVGRFNRFRSTNFEVLTPTNSTIFW 541  
 DB 436 THDGAEIELNGNDVDSGYDILNWHMGDAGITTFVKVGEYIFNSTKYELVLPKNSLFW 495  
 QY 542 NTSERLPHSVCTDVPPTGRTGFGVORBPICFDSIPCADGHVSRKPGRECEQCGEDVW 601  
 DB 496 NTSERLPHSVCTKLCAPGTGIRGIPGLOCCFACIPCADGVSVQKPGQREDCGEDW 555  
 QY 602 SNAQSECVLKEVEYLAYDEALGFTLVILSVFGAFVWLAVTAV 644  
 DB 556 SNAKSKVPLVFEFLAYEALGFTLVILSVFGAFVWLAVTAV 598

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RESULT 4
Q8TDUI PRELIMINARY; PRT; 365 AA.
AC Q8TDUI;
DT 01-JUN-2002 (TReMBLrel. 21, Created)
DT 01-JUN-2002 (TReMBLrel. 21, Last sequence update)
DE 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE Putative G-protein coupled receptor.
GN Name=GPCR;
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Takada S., Kadowaki S., Haga T., Takaesu H., Mitaku S.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
RL EMBL; AB083610; BAB9323.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0008067; F:metabotropic glutamate, GABA-B-like recepto. . .; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR000337; GPCR_Mgr.
DR Pfam; PF00003; 7cm_3; 1.
DR PRINTS; PR00248; GPCRMRGR.
DR PROSITE; PS50259; G_PROTEIN_RECEP_F3_4; 1.
KW Receptor.
SQ SEQUENCE 365 AA; 40920 MW; 9BFC4F8BFA873133 CRC64;

Query Match 35.7%; Score 1749; DB 2; Length 365;
Best Local Similarity 99.1%; Pred. No. 6.5e-115;
Matches 341; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 584 VSRKPGECRCQCEGDYWSNAQSECVLKEVEYLAYDEALGFTLVLSVFGAFVLAUTA 643
DB 22 VLRSIGERECCQCEGDYWSNAQSECVLKEVEYLAYDEALGFTLVLSVFGAFVLAUTA 81
QY 644 VYVHRHTPLVNASDWQGLFIQVLSLIIMLSSMLFIDKPHNMSCWAGQVTLALGFSCL 703
DB 82 VYVHRHTPLVNASDWQGLFIQVLSLIIMLSSMLFIDKPHNMSCWAGQVTLALGFSCL 141
QY 704 SCLIGKTSLSFLAYRISKSTOLTSMLPLRYKIIIVLSVLAETGICTAYLILEPPMYKN 763
DB 142 SCLIGKTSLSFLAYRISKSTOLTSMLPLRYKIIIVLSVLAETGICTAYLILEPPMYKN 201
QY 764 MESQNTKIILGNCISIEFLYSMGIDAFIALLCFLTFVARQLPDNYEGKCTITGMLV 823
DB 202 MESQNTKIILGNCISIEFLYSMGIDAFIALLCFLTFVARQLPDNYEGKCTITGMLV 261
QY 824 FFIWMSFVPLVSTKGKFMKAVEIFAILASSHGLGCIIPAPKCLIIILLRPERNTSEIVC 883
DB 262 FFIWMSFVPLVSTKGKFMKAVEIFAILASSHGLGCIIPAPKCLIIILLRPERNTSEIVC 321
QY 884 GRVSTTNCIQLTSFVSSSELNNTTVSLDDRLVLYMCEFLKQ 927
DB 322 GRVSTTNCIQLTSFVSSSELNNTTVSLDDRLVLYMCEFLKQ 365

RESULT 5
O70413 PRELIMINARY; PRT; 428 AA.
AC O70413;
DT 01-AUG-1998 (TReMBLrel. 07, Created)
DT 01-AUG-1998 (TReMBLrel. 07, Last sequence update)
DE 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE Putative pheromone receptor V2R2 (Fragment).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA Tissue=Vomeroneasal neurons;
RC Tissue=Vomeroneasal neurons;
RX MEDLINE=97436753; PubMed=9292726; DOI=10.1016/S0896-6273(00)80946-0;

RA Ryba N.J., Tirindelli R.;
RT "A new multigene family of putative pheromone receptors.";
RL Neuron 19:371-379(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC Tissue=Vomeroneasal neurons;
RA Ryba N.J.P., Tirindelli R.;
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF053989; AAC08416.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0008067; F:metabotropic glutamate, GABA-B-like recepto. . .; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR000337; GPCR_Mgr.
DR InterPro; IPR011500; NCD3G_GPCR.
DR Pfam; PF00003; 7cm_3; 1.
DR Pfam; PF07562; NCD3G; 1.
DR PRINTS; PR00248; GPCRMRGR.
DR PROSITE; PS50259; G_PROTEIN_RECEP_F3_4; 1.
KW Receptor.
FT NON_TER.
SQ SEQUENCE 428 AA; 47708 MW; EFB69A78F750E202 CRC64;

Query Match 35.2%; Score 1727; DB 2; Length 428;
Best Local Similarity 76.4%; Pred. No. 2.9e-113;
Matches 327; Conservative 40; Mismatches 61; Indels 0; Gaps 0;

QY 488 VILDNDGLKNGHYDVLNWLHDDGEISFVTVGRFNRSTNPELVIPNTSTIFWNTSSR 547
DB 1 VILDNDGLKNGHYDVLNWLHDDGEISFVTVGRFNRSTNPELVIPNTSTIFWNTSSR 60
QY 548 LPHSVCTDVCPTGRTGRGVQRPICCFDIPCADGHVSRKPKGRERCEOCEDYWSNAQKS 607
DB 61 RPDSECTQVCPGTRKIRGQPICCFDCIPCADGVSENFPGQRECDPCGEDDWSNAKS 120
QY 608 ECVLKEVEYLAYDEALGFTLVLSVFGAFVLAUTA VYVHRHTPLVNASDWQGLFIQV 667
DB 121 KCVPLKEVEYLAYDEALGFTLVLSVFGAFVLAUTA VYVHRHTPLVNASDWQGLFIQV 180
QY 668 SLIIMLSSMLFIDKPHNMSCWAGQVTLALGFSCLSLCLGKTSLSFLAYRISKSTOLT 727
DB 181 SVITVLSMLFIDKPHNMSCWAGQVTLALGFSCLSLCLGKTSLSFLAYRISKSTOLT 240
QY 728 SMHPLRYKIIIVLSVLAETGICTAYLILEPPMYKNMESQNTKIILGNCISIEFLYSMF 787
DB 241 SMSPIRYKIIIVLSVLAETGICTAYLILEPPMYKNMESQNTKIILGNCISIEFLYSMF 300
QY 788 GIDAFIALLCFLTFVARQLPDNYEGKCTITGMLVFFIWMSPVYLSLTKGKFMKAVE 847
DB 301 GFDVFLALLCFLTFVARQLPDNYEGKCTITGMLVFFIWMSPVYLSLTKGKFMKAVE 360
QY 848 IFAILASSHGLGCIIPAPKCLIIILLRPERNTSEIVCGRVSTTNCIQLTSFVSSSELNNT 907
DB 361 IFAILASSHGLGCIIPAPKCLIIILLRPERNTSEIVCGRVSTTNCIQLTSFVSSSELNNT 420
QY 908 TVSTVLDLDD 915
DB 421 AVSTVLDLDD 428

RESULT 6
CASR_BOVIN STANDARD; PRT; 1085 AA.
ID CASR_BOVIN
AC P35384;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Extracellular calcium-sensing receptor precursor (CaSR) (Parathyroid
DE Cell calcium-sensing receptor).
GN Name=CASR; Synonyms=GPRC2A, PCAR1;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
```

OX NCBI\_TaxID=9913;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Parathyroid; DOI=10.1038/366575a0;  
RX MEDLINE=94077182; PubMed=8255296; DOI=10.1038/366575a0;  
RA Brown E.M., Gamba G., Riccardi D., Lombardi M., Butters R., Kifor O.,  
RA Sun A., Hediger M.A., Lytton J., Hebert S.C.,  
RT "Cloning and characterization of an extracellular Ca (2+)-sensing  
RT receptor from bovine parathyroid.",  
RL Nature 366:575-580 (1993).  
CC -1- FUNCTION: Senses changes in the extracellular concentration of  
CC calcium ions. The activity of this receptor is mediated by a G-  
CC protein that activates a phosphatidylinositol-calcium second  
CC messenger system.  
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  
CC -1- SIMILARITY: Belongs to the G-protein coupled receptor 3 family.  
CC -----  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
DR EMBL; S67307; AAB29171.1; -;  
DR F1R; S40476; S40476.  
DR HSP; P23385; LEWT.  
DR InterPro; IPR001828; ANF receptor.  
DR InterPro; IPR000068; Ca\_sens\_receptor.  
DR InterPro; IPR000337; GPCR Mgr.  
DR Pfam; PF00003; 7tm 3; 1.  
DR Pfam; PF01094; ANF receptor; 1.  
DR PRINTS; PR00248; GPCRMR.  
DR PROSITE; PS00979; G\_PROTEIN\_RECP\_F3\_1; 1.  
DR PROSITE; PS00980; G\_PROTEIN\_RECP\_F3\_2; 1.  
DR PROSITE; PS00981; G\_PROTEIN\_RECP\_F3\_3; 1.  
DR PROSITE; PS0259; G\_PROTEIN\_RECP\_F3\_4; 1.  
KW G-protein coupled receptor; Glycoprotein; Signal; Transmembrane.  
FT SIGNAL 1 19 Potential.  
FT CHAIN 20 1085 Extracellular calcium-sensing receptor.  
FT DOMAIN 20 613 Extracellular (Potential).  
FT TRANSMEM 614 636 1 (Potential).  
FT DOMAIN 637 650 Cytoplasmic (Potential).  
FT TRANSMEM 651 671 2 (Potential).  
FT DOMAIN 672 682 Extracellular (Potential).  
FT TRANSMEM 683 701 3 (Potential).  
FT DOMAIN 702 725 Cytoplasmic (Potential).  
FT TRANSMEM 726 746 4 (Potential).  
FT DOMAIN 747 770 Extracellular (Potential).  
FT TRANSMEM 771 793 5 (Potential).  
FT DOMAIN 794 806 Cytoplasmic (Potential).  
FT TRANSMEM 807 829 6 (Potential).  
FT DOMAIN 830 837 Extracellular (Potential).  
FT TRANSMEM 838 863 7 (Potential).  
FT DOMAIN 864 1085 Cytoplasmic (Potential).  
FT CARBOHYD 91 91 N-linked (GlcNAc... ) (Potential).  
FT CARBOHYD 131 131 N-linked (GlcNAc... ) (Potential).  
FT CARBOHYD 262 262 N-linked (GlcNAc... ) (Potential).  
FT CARBOHYD 288 288 N-linked (GlcNAc... ) (Potential).  
FT CARBOHYD 401 401 N-linked (GlcNAc... ) (Potential).  
FT CARBOHYD 447 447 N-linked (GlcNAc... ) (Potential).  
FT CARBOHYD 469 469 N-linked (GlcNAc... ) (Potential).  
FT CARBOHYD 489 489 N-linked (GlcNAc... ) (Potential).  
FT CARBOHYD 542 542 N-linked (GlcNAc... ) (Potential).  
FT CARBOHYD 595 595 N-linked (GlcNAc... ) (Potential).  
SQ SEQUENCE 1085 AA; 121170 MW; 5D66DE89CD13B47 CRC64;  
Query Match 34.6%; Score 1695.5; DB 1; Length 1085;  
Best Local Similarity 39.3%; Pred. No. 1.7e-110;  
Matches 350; Conservative 173; Mismatches 323; Indels 45; Gaps 15;  
QY 53 LVIGGLFPIDSRIPANESI-LEPASAKCEGFNFRWNKAMIIHMIKINKKIDLPNI 111

Db 33 IILGGLFPIHFGVAVKQDLSRPSVECIIRNFRGRWLQAMFAIEBINSFALLPNN 92  
QY 112 TLGYOIFDPTCTTISVRAVLVFLAQE---ENRPNFRNSTGAPFA--GIVGAGSFLSV 166  
Db 93 TLGYRIFDPTCNVTSKALEATLSFVAQNKIDSLNLFDFCMCSHIFSTIAVAGTSGIST 152  
QY 167 PASRILGLYLPQVGYTSTCVILSDKYQPPSYLRVIASDKIQSKAVVKKRQIHFGWVWGA 226  
Db 153 AVANLGLFYIPQVSYASSRLLSNKQPKSLRTIPNDEHQATAMADIIIEFRWNWGT 212  
QY 227 IAADDYGYKVTPEKMEKANLVAFSSETTPKVSNEKQKAVAKVTSTAKVILVYT 286  
Db 213 IAADDYGRPGIEKFEAEERDICIDFSSELISQYSDSEKIQQVVEIQNSTAKVIVFS 272  
QY 287 SDIDLSLFVLEMIHNITDRWIAEMITSALIAKPEVFPYFGGTIGPATPRSVPLGLK 346  
Db 273 SPDLLEPLIKEIVRRNITGRILWASEANASSLIAMPFYHVVGGTIGRLKAGQIPGR 332  
QY 347 EFLYDHPNKPNDVLTITFEWQAFNC-TWPNSSVPYVNDVRNMTGKEDRLYDSQ-- 403  
Db 333 EFLQVHPKSVHNGFAKEFEETFNCHLQEGAKGLPVD--TFLRGHEEGCARLSNPT 390  
QY 404 ----LCTGEEKLEDKNTVLTQSRLRTKQCKQAVYAIAGLDHLSRCQGGQPGSGNOQ 459  
Db 391 AFRPLCTGEENISSVETPTMDYTHLRISVNVYLAIVSYIAHALQDIYTCIPGRGLF -TNGS 449  
QY 460 CAYIPTDFQWLMYMKIKPKSHEDKWLIDNDGLKNGHVDVNLNHL-DGEISFVT 518  
Db 450 CADIKKVAWQVLRHLNFTSNMGEQVTFDECDGLA-GNYIINHLWSPDGSIVFKB 508  
QY 519 VGRFNRSTNPFELVITNSTIFWNTSESSLRHSVCTDVCPPGTGRGFQREICCPDSTP 578  
Db 509 VGVYVYAKGERLFINDEKILMSGFSREVPSNCRDCLACTRKGIIIEGETCCPECVE 568  
QY 579 CADGHVSRKPERECCQCGEDYWSNAKSECVLKEVYLAIDEALGFTLVILSVGAFVV 638  
Db 569 CPDGEYSDETDASACDKCPDDPFSNENHTSCIAKEIEFLSWTEPFEGIALTLFAVLGIFLT 628  
QY 639 LAVTAVYVHHTPLVNASDQGLIQLVSLIIMLLSSMLFIDKPHNSCMAGVTLAG 698  
Db 629 AFVLGVFKFRNTPIVKATNRRELSYLLFSLCCFSSSLFFIEGPDQWTCRLRQPAFGIS 688  
QY 699 FSLCISLIGKTSLSFLAYRISKSTQLTSMHPLYRK-----IIVLSVLAETIGCT 750  
Db 689 FVLICISLIVKTRVLLVF---EAKIP-TSFH--RKWGLNLQFLVFLCTFMQIVICA 741  
QY 751 AYLIILEPPMVYKNMESQNTKILGCNEISIEFLYSMPGIDAFLLCLFUTTFVARQLPN 810  
Db 742 IWLNTAPPSSVYRNHELEBIIFITCHEGSLMALGFLIGVTCLLAAICFFFAFKSKRLPEN 801  
QY 811 YVEGKICITFGLVPEIIVMSFPVYLSYKGFMAVEIFAILASSHGLIGCIPAPKCLII 870  
Db 802 FNEAKFITFSMLIFFIWMISFIPAYASTYGFVSAVEVIAILASSFGLLACIIPFNKVYII 861  
QY 871 LIRPERNTSEIVCGRVSTTDCIQLTSAFV-----SSELNNTVST 911  
Db 862 LFKPSRNTIEEV--RCSTAAHAFKVAARATLRSSVRSQRSSSLGGSTGST 910  
RESULT 7  
Q8COM6  
ID Q8COM6 PRELIMINARY; PRT; 476 AA.  
AC Q8COM6;  
DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Mus musculus adult male testis cDNA, RIKEN full-length enriched  
DE library, clone:493425M15 product:similar to PUTATIVE PHEROMONE  
DE RECEPTOR V2R2, full insert sequence.  
GN Name=493425M15Rik;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;



DR PROSITE; PS00980; G\_PROTEIN\_RECP\_F3\_2; 1.  
DR PROSITE; PS00981; G\_PROTEIN\_RECP\_F3\_3; 1.  
DR PROSITE; PS00982; G\_PROTEIN\_RECP\_F3\_4; 1.  
KW Receptor.  
SQ SEQUENCE 1079 AA; 120830 MW; 50A2D026AE65CE81 CRC64;

Query Match 34.5%; Score 1691.5; DB 2; Length 1079;

Best Local Similarity 38.0%; Pred. No. 3.3e-110;

Matches 352; Conservative 181; Mismatches 332; Indels 61; Gaps 17;

QY 18 LAFWM--AELGSEAKSEKEERCRLLGKCVDAENSHLVIGLFPDSDRTIPANESI-LE 74

DB 11 LALWSSAYGPQRAQKGD-----IILGLLPIHFGVAAKQDLKSR 54

QY 75 PASAKCEGFNFRWAKMIHKEINKRKDILPNITLGYQIFDCTFISKEVAVLVF 134

DB 55 PESVEICIRYFRWLOQAMPALEINSPLPNMTLGYRIFDCTVSKALEATLSP 114

QY 135 LTQGE---ENRPNFRNSTGAPPA--GIVGAGGSFLVPASRIILGLYLPQVGYTSCVIL 189

DB 115 VAQNKIDSLNLDKFCNCEKIPSTIAVVGATGSGVSTAVANLLGLFVLPQVSYASSRLL 174

QY 190 SDKQVPSYLRVITASKIQSAVVKVIOHFGWVWCAIAADDDYKGVKTKPKKMSAN 249

DB 175 SNKNQYKSFLETTIPNDEHQATMADIIEYFRNWNVGTIAADDDYGRPGIEKFEAEERD 234

QY 250 LCVAPSETIPKVSNEKMKAVKAVTSTAKVLTYSIDILSLFVLEMIHNTDRTWI 309

DB 235 ICIDFSELISQYDESEIQOVVEIQNSTAKVIVFSSGPDLEPLKEIVRRNITGRILW 294

QY 310 ATEAWITSALIAKPEYFPFGTIGPATRSVPLGLKEFLYDVHPNKPNDVLTIFWOT 369

DB 295 ASEAWASSLLAMPEYFHVVGITIGLXAGQIPGFREFLVKHPKSVHNGFAKEFWEE 354

QY 370 AFNCTWPNSS---VPYVNDVRNMTKEBRLYDMSD---QLCTGEKLEBRLNXYLDTQ 423

DB 355 TFNCHLQEGAKGLPVDYTFVRSHEEG--GNRLNLSSTAFRLPCTGDNINSVPTVMDYEH 413

QY 424 LRITKCKQAVYAIAGHLHLSCQSGQGFSGNQOCQAVIPTDFWQLVYMKIKFKSH 483

DB 414 LRISYNYLAVYSIAHALQDIYTCLEPGLF--TNGSCADIKKVAQVQLKHLNFTNN 472

QY 484 EDKWLIDDDGDLKNGHYDLVNLHLLD--DEGEISFVTVGRNFRSTFELVPIPTNTPFN 542

DB 473 MGEQVTFDECDLV--GNYSIINHLSPEDGSIVFKEVYVYVAKGERLFINEEKILMS 531

QY 543 TESSRLPHSVCTVCPPTGTRGVQREPTCCFDSIPCADGHVSRKPGRECBQCGDYWS 602

DB 532 GFSREVPFNSCRDCQAGTRKGIIEGEPTCCFCEVCEPDGEVSGETDASACDKCPDFWS 591

QY 603 NAKSCSVLKEVEYLADEALGFTLVLSVFGAFVVLAVTAVYVIRHTPLYNASDWQLG 662

DB 592 NENHTSCIAKEISFLAWTEPFGIALTFALVGLFGLFVGLVFKRNTPIVAKATRELS 651

QY 663 FLIQVSLIIMLSSMLFDKPHNWSQWAGQVTLALGFSCLSLCLGTSLSFLAYRISK 722

DB 652 YLLFSLCCFSSSLFIEGPQDWTCLRQPAFGISFVICISILVKTNRVLLF---EA 708

QY 723 KTLQTSMLPYRK-----IIVLSVLAEGICITAYLILEPPMVYKMMESQNTKIILG 774

DB 709 KIP-TSFH---RKWGLNLQFLVFLCTFMQILICIILWLTAPPSSRYRNEHEDEIIFT 764

QY 775 CNEISIEFLYSMEGIDAFLLALCLFLTFVARQLPDNYEKGCTITGMLVFFIWMSPV 834

DB 765 CHEGSLMALGSLIGYTCLLAAICFFPAFKSRKLPENFEAKFTTFGMLFIIVWISFIPA 824

QY 835 YLSTGKFKMAVIFAILASSHGLLICIPAPKCLIIILRPENTSVICGRVSTTDCNQ 894

DB 825 YASTYKGFSAVEVIAILAAAFGLLACIPFNKYIILFKFSRNTIEEV--RSTAAHAPK 882

QY 895 LTSAFV-----SSSELNNTVS 910

DB 883 VAARATLRPNISRKSSSLGGSTGS 908

## RESULT 9

ID	CASR	RAT	STANDARD;	PRT;	1079	AA.
AC	P48442;					
DT	01-FEB-1996 (Rel. 33, Created)					
DT	01-FEB-1996 (Rel. 33, Last sequence update)					
DT	25-OCT-2004 (Rel. 45, Last annotation update)					
DE	Extracellular calcium-sensing receptor precursor (CaSR) (Parathyroid Cell calcium-sensing receptor).					
GN	Name=CaSR; Synonyms=Gprc2a, Pcarl;					
OS	Rattus norvegicus (Rat).					
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.					
OX	NCBI_TaxID=10116;					
RP	SEQUENCE FROM N.A.					
RC	STRAIN=Sprague-Dawley; TISSUE=Kidney outer medulla;					
RX	MEDLINE=95116508; PubMed=7816802;					
RA	Riccardi D., Park J., Lee W., Gamba G., Brown E.M., Hebert S.C.;					
RT	"Cloning and functional expression of a rat kidney extracellular calcium/polyvalent cation-sensing receptor.";					
RL	Proc. Natl. Acad. Sci. U.S.A. 92:131-135(1995).					
RN	[2]					
RP	SEQUENCE OF 1-294 FROM N.A.					
RC	STRAIN=Wistar;					
RX	MEDLINE=95241465; PubMed=7724534;					
RA	Ruat M., Snowman A.M., Snyder S.H.;					
RT	"Calcium sensing receptor: molecular cloning in rat and localization to nerve terminals.";					
RL	Proc. Natl. Acad. Sci. U.S.A. 92:3161-3165(1995).					
CC	-!- FUNCTION: Senses changes in the extracellular concentration of calcium ions. The activity of this receptor is mediated by a G-protein that activates a phosphatidylinositol-calcium second messenger system.					
CC	-!- SUBCELLULAR LOCATION: Integral membrane protein.					
CC	-!- SIMILARITY: Belongs to the G-protein coupled receptor 3 family.					
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a> or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> ).					
CC	EMBL; U10354; AAC52149.1; -					
DR	EMBL; U20289; AAC52195.1; -					
DR	PIR; I59362; I59362.					
DR	HSP; P23385; LEWK.					
DR	RGD; 2277; CaSR.					
DR	InterPro; IPR001828; ANF receptor.					
DR	InterPro; IPR00068; Ca_sens receptor.					
DR	InterPro; IPR000337; GPCR_Mgr.					
DR	Pfam; PF00003; 7tm_3; 1					
DR	Pfam; PF01094; ANF_receptor; 1					
DR	PRINTS; PR00248; GPCRMR.					
DR	PROSITE; PS00379; G_PROTEIN_RECP_F3_1; 1.					
DR	PROSITE; PS00380; G_PROTEIN_RECP_F3_2; 1.					
DR	PROSITE; PS00381; G_PROTEIN_RECP_F3_3; 1.					
DR	PROSITE; PS00359; G_PROTEIN_RECP_F3_4; 1.					
KW	G-protein coupled receptor; Glycoprotein; Signal; Transmembrane.					
FT	SIGNAL 1 19 Potential.					
FT	CHAIN 20 1079 Extracellular calcium-sensing receptor.					
FT	DOMAIN 20 612 Extracellular (Potential).					
FT	TRANSMEM 613 635 1 (Potential).					
FT	DOMAIN 636 649 Cytoplasmic (Potential).					
FT	TRANSMEM 650 670 2 (Potential).					
FT	DOMAIN 671 681 Extracellular (Potential).					
FT	TRANSMEM 682 700 3 (Potential).					
FT	DOMAIN 701 724 Cytoplasmic (Potential).					
FT	TRANSMEM 725 745 4 (Potential).					



FT	DOMAIN	746	769	Extracellular (Potential).
FT	TRANSMEM	770	792	5 (Potential).
FT	DOMAIN	793	805	Cytoplasmic (Potential).
FT	TRANSMEM	806	828	6 (Potential).
FT	DOMAIN	829	836	Extracellular (Potential).
FT	TRANSMEM	837	862	7 (Potential).
FT	DOMAIN	863	1079	Cytoplasmic (Potential).
FT	CARBOHYD	90	90	N-linked (GlcNAc. .) (Potential).
FT	CARBOHYD	130	130	N-linked (GlcNAc. .) (Potential).
FT	CARBOHYD	261	261	N-linked (GlcNAc. .) (Potential).
FT	CARBOHYD	287	287	N-linked (GlcNAc. .) (Potential).
FT	CARBOHYD	386	386	N-linked (GlcNAc. .) (Potential).
FT	CARBOHYD	446	446	N-linked (GlcNAc. .) (Potential).
FT	CARBOHYD	468	468	N-linked (GlcNAc. .) (Potential).
FT	CARBOHYD	488	488	N-linked (GlcNAc. .) (Potential).
FT	CARBOHYD	541	541	N-linked (GlcNAc. .) (Potential).
FT	CARBOHYD	594	594	N-linked (GlcNAc. .) (Potential).
SQ	SEQUENCE	1079	AA; 120867 MW; D7664550361F9736 CRC64;	

Query Match

Best Local Similarity 34.5%; Score 1690.5; DB 1; Length 1079;

Matches 352; Conservative 181; Mismatches 332; Indels 61; Gaps 17;

Qy	18	LAFW--AELGSEAKEKEBEERTCLLGKCVDAENHSLVIGLFPIDSDTIIPANESI-LE 74
Db	11	LALAWHSSAYGPDQRAQKGD-----IILGLFPIHFGVAAKQDQLKSR 54
Qy	75	PASAKCGFNQFRWWMKAMHMIKEINKRKDILPNITIGYQIFDFCTFISKSVEAVLVP 134
Db	55	PESVCEIYRFRGFRQAMIFAIEEINSPSLPNMTLGYRFDTCNTVSKALSATLSF 114
Qy	135	LTGQE---ENRPNFRNSTGAPPA--GIVGAGGSFLSPASRIILGLYLPQVGVTCTCVIL 189
Db	115	VAQNKIDSLNDFECNCESHIPSTIAVVGATGSGVTAVANLLGLFYIIOVSYASSRLL 174
Qy	190	SDKYQPSYLRVITASDKIQSKAVVVKRIQHPGWWVGAIAADDYGYKGVKTFKKMESAN 249
Db	175	SNKNQYSKFLRTIPNDSHQATAMADIIEYFRWNVGTIAADDYGRPGIEKFRFEAEERD 234
Qy	250	LCVAFSEITPKVSYNEKQKAVKAVKTSTAKVILVLTSDILSLFLVLEMIHNITDRTWI 309
Db	235	ICIDFSELISQYDEEIQQVVRVQNSTAKVILVWFSSGPDLEPLKEIVRRNITRIWL 294
Qy	310	ATEAWITSALIAKPEYFPFGTTIGFATPRSVIPGLKEFLYDVHPNKPNDVLTITFQWT 369
Db	295	ASEAWSSLLAMPPEYFHVGGTIGLKGAGQIPGFRFLQKVPKPSVHNGFAKEFWE 354
Qy	370	AFNCTWPNSS---VPYVNDVHRVNMVTKEDRLYDMSD---QLCTGEBKLEDLKNVYLDTSQ 423
Db	355	TFNCHLQEGAKGPLPVDTVFVSHEEG--GNRLNLSSTAFRPLCTGDNINSVETPYMDYEH 413
Qy	424	LRITKQCKQAVYATAHGLDHLRSQCGQPGFNQOCAYIPTDFWQLMYMYKKEIKFKSH 483
Db	414	LRISYNVLAIVYSTAHALQDIYITCLPGRGLF--TNGSCADIKKVEAWQVLKHLHLNFTNN 472
Qy	484	EDKWVILDDGDLKNGHYDVLNWLHD--DEGEISFTVTGVRNFRSTNFFELVPTNSTFIWN 542
Db	473	MGEQVTFDECGDLV--GNYSIINWLSPEDGSIYFKEVGYNYVAKKGERLFINKEKILMS 531
Qy	543	TESSRLPHSVCTVCPGTCGRGVFQRPBPCFDSIPCADGHVSRKPGRECECGEDYWS 602
Db	532	GFSREVFPNSCRDCAQTRKGIIEGPTCCFCEVCEPDGEGSETDASACDKCPDFFWS 591
Qy	603	NAQSECVLKEVEYLAYDEALGFTILVLSVFGAFVVLAVTAVVIRHPTLYNASDWQLG 662
Db	592	NENHTSCTIAKEIEFLAWTEPFGIALTLFAVLGIFLTAFLGVFIKFRNTPIVKATNRELS 651
Qy	663	FLIQVSLIIMLLSMLFIDKPHNWSMAGQVTLALGFSCLGKTSLSFLAYRISKS 722
Db	652	YLLFLSLCCFSSSLFFIGEPQDWTCRLRQAPAGISFVLICISILVKTNRVLLVP---EA 708
Qy	723	KTQLTSMHPLYRK-----IIVLSVLAIEGICTAYLILEPMPYVKMESQNTKIILG 774

Db	709	KIP-TSFH---RKWGLNLQFLFLCTPMQILICIWIYLTAPPSSYRNHELEDEIFIT 764	
Qy	775	CNEISIEFLYSNMGIDAFILALACELTTFVAROLPDNYEGKCTTFCGLVLPFIWMSFVPV 834	
Db	765	CHEGSLMALGSLIGTYTCLLAAICFFAFKSRKDPENFNEAKFTTFSLMFIFFIWISSIP 824	
Qy	835	YLSTKGFKFMAYEIPAILASSHGLLCIPAPKCLIIILLPERNTSIVCORGVSTTDCIQ 894	
Db	825	YASTYKGFSAVEVIAALAAASFGLLACIFFNKVYIILFKPSRNTIEEV--RSSTAHAHFK 882	
Qy	895	LTSAPV-----SSELNNTTVS 910	
Db	883	VAARATLRPNISRKRSLSLGGSTGS 908	
RESULT 10			
ID	Q8J104	PRELIMINARY; PRT; 1027 AA.	
AC	Q8J104;		
DT	01-OCT-2002 (TREMBlrel. 22, Created)		
DT	01-OCT-2002 (TREMBlrel. 22, Last sequence update)		
DT	01-WAR-2004 (TREMBlrel. 26, Last annotation update)		
DE	Calcium polyvalent cation receptor/salinity sensing protein.		
OS	Squalus acanthias (Spiny dogfish).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;		
OC	Elasmobranchii; Squalia; Hynosaqualia; Squaliformes; Squaloidei;		
OC	Squalidae; Squalus.		
OX	NCBI_TaxId=7797;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Kidney;		
RX	MEDLINE=22103704; PubMed=12093923; DOI=10.1073/pnas.152294399;		
RA	Nearing J., Betka M., Quinn S., Hentschel H., Elger M., Baum M.,		
RA	Bai M., Chattopadhyay N., Brown E.M., Hebert S.C., Harris H.W.;		
RT	"Polyvalent cation receptor proteins (Cars) are salinity sensors in fish."		
RL	Proc. Natl. Acad. Sci. U.S.A. 99:9231-9236 (2002).		
DR	EMBL; AF406649; AAM7700.1; --		
DR	HSSP; P23385; 11SS.		
DR	GO; GO:0015020; C:membrane; IEA.		
DR	GO; GO:0008067; F:metabotropic glutamate, GABA-B-like recepto. .; IEA.		
DR	GO; GO:0004872; F:receptor activity; IEA.		
DR	InterPro; IPR001828; ANF receptor.		
DR	InterPro; IPR000068; Ca_sens receptor.		
DR	InterPro; IPR001337; GPCR Mgr.		
DR	InterPro; IPR011500; NCD3G_GPCR.		
DR	Pfam; PF00003; 7cm_3; 1.		
DR	Pfam; PF01094; ANF receptor; 1.		
DR	Pfam; PF07562; NCD3G; 1.		
DR	PRINTS; PR00592; CASENSINGR.		
DR	PRINTS; PR00248; GPCRMRG.		
DR	PROSITE; PS00979; G_PROTEIN_RECEP_F3_1; 1.		
DR	PROSITE; PS00980; G_PROTEIN_RECEP_F3_2; UNKNOWN_1.		
DR	PROSITE; PS00981; G_PROTEIN_RECEP_F3_3; 1.		
DR	PROSITE; PS00259; G_PROTEIN_RECEP_F3_4; 1.		
KW	Receptor.		
SQ	SEQUENCE 1027 AA; 114412 MW; 189FF1E323B5B7C7 CRC64;		
Query Match 34.4%; Score 1688.5; DB 2; Length 1027;			
Best Local Similarity 38.6%; Pred. No. 5e-110;			
Matches 346; Conservative 176; Mismatches 323; Indels 51; Gaps 14;			
Qy	53	LVIGLFPIDSDRTIPANESI-LEPASAKCGFQFQPRWKMAMHKIKRKKDILPNI 111	
Db	36	IILGLFPIHFGVAAKQDQLKSRPEATKIRYNFRGFRWLQAMIFAIEEINNSMTFLPNI 95	
Qy	112	TLGYQIFDCTFTISKSVEAVLVLFTGQE---ENRPNFRNSTGAPPA--GIVGAGGSFLSV 166	
Db	96	TLGYRFDTCNTVSKALEATLSFAQNKIDSLNDFECNCDHIPSTIAVVGATGSGIST 155	
Qy	167	PASRIILGYLPQVGVTSTCVILSDKYQPSYLRVITASDKIQSKAVVVKRIQHPGWWVGA 226	
Db	156	AVANLLGLFYIPQVSAYSSRLLSNKNYKAFILRTIPNDEQQATAMABIEHFQWNWGT 215	





"Mutations in the Ca(2+)-sensing receptor gene cause autosomal dominant and sporadic hypoparathyroidism."; Hum. Mol. Genet. 5:601-606(1996). [12]

VARIANT FHH ARG-174.

RP MEDLINE=97442275; PubMed=9298824; DOI=10.1002/(SICI)1098-1004(1997)10:3<233::AID-HUM9>3.3.CO;2-G; Ward B.K., Stuckey B.G.A., Gutteridge D.H., Laing N.G., Pullan P.T., Ratajczak T.; J. Clin. Endocrinol. Metab. 84:3036-3040(1999). [14]

"A novel mutation (L174R) in the Ca2+-sensing receptor gene associated with familial hypocalcemic hypercalcemia."; Hum. Mutat. 10:233-235(1997). [13]

VARIANT FHH VAL-616.

RP MEDLINE=99415602; PubMed=10487661; DOI=10.1210/jc.84.9.3036; Stock J.L., Brown R.S., Baron J., Coderre J.A., Mancilla E., De Luca F., Ray K., Mericq M.V.; J. Clin. Endocrinol. Metab. 84:3036-3040(1999). [14]

"A novel mutation in Ca2+-sensing receptor gene in familial hypocalcemic hypercalcemia."; Endocrine 15:277-282(2001).

CC -!- FUNCTION: Senses changes in the extracellular concentration of calcium ions. The activity of this receptor is mediated by a G-protein that activates a phosphatidylinositol-calcium second messenger system.

CC -!- SUBCELLULAR LOCATION: Integral membrane protein.

CC -!- ALTERNATIVE PRODUCTS:

CC Event-Alternative splicing; Named isoforms=2;

CC Name=1;

CC IsoId=P41180-1; Sequence=Displayed;

CC Name=2;

CC IsoId=P41180-2; Sequence=VSP\_002035;

CC -!- TISSUE SPECIFICITY: Found in kidney, but not in brain, lung, liver, heart, skeletal muscle, or placenta.

CC -!- DISEASE: Defects in CASR are the cause of familial hypocalcemic hypercalcemia, type 1 (FHH) [MIM:145980]; in which the receptor has reduced activity. FHH is characterized by altered calcium homeostasis. Affected individuals exhibit mild or modest hypercalcemia, relative hypocalcemia, and inappropriately normal PTH levels.

CC -!- DISEASE: Defects in CASR are the cause of neonatal severe primary hyperparathyroidism (NSHPT) [MIM:239200]; in which the receptor has reduced activity. NSHPT is a rare autosomal recessive life-threatening disorder characterized by very high serum calcium concentrations, skeletal demineralization, and parathyroid hyperplasia. In some instances NSHPT has been demonstrated to be the homozygous form of FHH.

CC -!- DISEASE: Defects in CASR are the cause of autosomal dominant hypocalcemia (ADH) [MIM:601198]; in which the receptor is activated at subnormal Ca(2+) levels.

CC -!- DISEASE: Defects in CASR are the cause of autosomal dominant hypoparathyroidism (FHH) [MIM:146200]. FHH is characterized by hypocalcemia and hyperphosphatemia due to inadequate secretion of parathyroid hormone. Symptoms are seizures, tetany and cramps.

CC -!- SIMILARITY: Belongs to the G-protein coupled receptor 3 family.

CC -----

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CC -----

DR EMBL; X81086; CAA56990.1; -.

DR EMBL; U20759; AAA86503.1; -.

DR EMBL; U20760; AAA86504.1; -.

DR EMBL; D50855; BAA09453.1; -.

DR EMBL; S83176; AAB46873.1; -.

DR EMBL; S79217; AAB35262.2; -.

DR EMBL; S68032; AAB29413.2; ALT\_SEQ.

DR EMBL; S68033; AAB29414.1; -.

DR EMBL; S68036; AAB29415.1; -.

DR EMBL; S81755; AAD14370.1; -.

DR HSSP; P23385; LEWK.

DR Genew; HGNC:1514; CASR.

DR MIM; 601199; -.

DR MIM; 145980; -.

DR MIM; 233200; -.

DR MIM; 601198; -.

DR MIM; 146200; -.

DR GO; GO:0005887; C:integral to plasma membrane; TAS.

DR GO; GO:0004930; F:G-protein coupled receptor activity; TAS.

DR GO; GO:0004435; F:phosphoinositide phospholipase C activity; TAS.

DR GO; GO:0006874; P:calcium ion homeostasis; TAS.

DR GO; GO:0005513; P:calcium ion sensing; TAS.

DR GO; GO:0007635; P:chemosensory behavior; TAS.

DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; TAS.

DR GO; GO:0009653; P:morphogenesis; TAS.

DR GO; GO:0001503; P:ossification; TAS.

DR InterPro; IPR001828; ANF\_receptor.

DR InterPro; IPR000068; Ca\_gens\_receptor.

DR InterPro; IPR000337; GPCR\_Mgr.

DR Pfam; PF00003; 7tm3; 1.

DR Pfam; PF01094; ANF\_receptor; 1.

DR PRINTS; PRO0248; GPCRMR.

DR PROSITE; PS00979; G\_PROTEIN\_RECP\_F3\_1; 1.

DR PROSITE; PS00980; G\_PROTEIN\_RECP\_F3\_2; 1.

DR PROSITE; PS00981; G\_PROTEIN\_RECP\_F3\_3; 1.

Query Match 34.4%; Score 1687.5; DB 1; Length 1078;

Best Local Similarity 38.0%; Pred. No. 6.3e-110;

Matches 353; Conservative 179; Mismatches 333; Indels 63; Gaps 18;

QY 18 LAFLW--AELGSEAKEEKEERTCRLLGKCVDAENHSLVIGGLFPDLSRIPANESI-LE 74

DB 11 LALTWHTSAYDPDQRAQKGD-----IILGGLFPIHFGVAAKQDILKSR 54

QY 75 PASACEGFNFQFRWKMAMHMKRKRKDLIPNITLGYQIFDFTCTTISKSVEAVLVF 134

DB 55 PSFVCEIRYFGRFLQMIFAIBEINSPALLPNLTIGYRIFDTCNTVSKALEATLSP 114

QY 135 LFGQE---ENRPNFRNSTGAFFA--GIVGAGGSFLSVPASRLILGYLPQVGTSTCVIL 189

DB 115 VAQNKIDSLNLDEFNCSEHIPSTIAVVGATGSGVSTAVANLLGLFYIPQVSASSRLL 174

QY 190 SDKYQPPSVLRVIAADKIQSKAVVXRIQHFQWVWVCAIAADDDYKGYKVTFKKESAN 249

DB 175 SNKNQFKSFLRTIPNDEHQATAMADIEYFRWNWVGTIAADDDYGRPGIEKPREAEERD 234

QY 250 LCVAFSEITPKVYSNEKMKAVKAVKTAKVTLVLTSDTDLSLFVLEMHNTITRTWI 309

DB 235 ICIDFSELLSQSDEEIQHVVEVTONSTAKVIVFSSGPDLEPLKEIVERNITGKLWL 294

QY 310 ATEAMITGALIAKPYFPYFGTIGFATPRSVIPGLKEFLYDVHPNKPDPNLTIEFWQT 369

DB 295 ASEAWASSSLIAMPQYFHVVGTTIGFALKAGQIPGFRFLKVKVPRKSVHNGFAKEFWEE 354

QY 370 AFNC--TPWNSVYPNVNDRVNMVTKGK---DRLYDMSD---QLCTGKLELDKNVYLDTS 422

DB 355 TPNCLQEGAKGLPVD--TFLRGHEESGDRFSNSSTAFRPLCTGDNISSTVETPYIDYT 412

QY 423 QLRIKTKCKQAYVAYTAIGHDLHSRQEGQPGFGSNQCCAYIPTFFDFWQLMYMKKIKFKS 482

DB 413 HLRSISVNYLVAVYSIAHALQDIYVCLPGRGLP--TGNSCADIKKVEAWQLKHLHLNFTN 471

QY 483 HDKWKVILDDNGDLKNGHYDVNLWNHLD--DEGISFTVTVGRFNRPRSTNPFELVITPNSTIFW 541

DB 472 NMGEQVTFDECGDLV--GNYSIINWHLSPEDGSGIVFKEVGYNYVYAKKGERLFINEEKILW 530







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786 TEAKFITPSMLFFIIVWISFIPAYFSTYGRKFSVAVEVIAIALASSFGLLACIFENKVIIL 845
QY 872 LRPERNTSEIYCVGRVSTTDCIQLTS 897
Db 846 FKPSRNTIEEV--RCSTAASHFKVAA 869

RESULT 15
Q6XAF3
ID Q6XAF3 PRELIMINARY; PRT; 941 AA.
AC Q6XAF3;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Calcium polyvalent cation receptor 2.
OS Salmo salar (Atlantic salmon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.
OX NCBI_taxID=8030;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RA Nearing J.A.; Harris W.;
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY245443; AAP79923.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0008067; F:metabotropic glutamate, GABA-B-like recepto...; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR001828; ANF receptor.
DR InterPro; IPR000068; Ca sens receptor.
DR InterPro; IPR000337; GPCR_MgR.
DR InterPro; IPR011500; NCD3G_GPCR.
DR Pfam; PF00003; 7tm_3; 1.
DR Pfam; PF01094; ANF receptor; 1.
DR Pfam; PF07562; NCD3G; 1.
DR PRINTS; PR00592; CASSENSINGR.
DR PRINTS; PR00248; GPCR_MGR.
DR PROSITE; PS00979; G_PROTEIN_RECEP_F3_1; 1.
DR PROSITE; PS50253; G_PROTEIN_RECEP_F3_4; 1.
KW Receptor.
SQ
SEQUENCE 941 AA; 106072 MW; C72B91C0029DF27 CRC64;

Query Match
Best Local Similarity 38.2%; Score 1629.5; DB 2; Length 941;
Matches 332; Conservative 168; Mismatches 317; Indels 49; Gaps 13;

QY 53 LVIGGLPPIIDSRITIPANESI-LEPAKACEGFNFQFRWKKAMIMHKEINKRKDILPNI 111
Db 32 ILLGLPMPHFGVTSKQDLAARPESTECVRYNFRGFRWLQAMI PAIEBINNSLTLPNI 91
QY 112 TLGVQIEDTCFTISKVSEAVLVLTLQGE---ENRPNFRNSTGAPPA--GIVAGSGFLSV 166
Db 92 TLGVRIEDTCTNTSKALEATLSVAQNKIDSLNDEFNCNTHIPSTIAVVGSGSAVST 151
QY 167 PASRILGLYLPQGVGTSCVILSDKYQPSYLRVLTASDKIOSKAVVKRIQHFGVWVGA 226
Db 152 AVANLLGLFVLPQISVASSRLSNKNQKFSFRTIPTDEHQATADIIDYQWNWVIA 211
QY 227 IAADDDYKGYKVTPEKMEKANLVAFSETIPKYSNEMQKAKVAKTSTAKVILVYT 286
Db 212 VASDDYGRPGIEKEEMEERDICHLSSELISQYFEWQIQGLVGRIENTSSAKVIVVFA 271
QY 287 SDIDLSLFVLEMIHMTDRTWATWITSAWITSALIAKPEYFPFGTIGPATPRSVIPGLK 346
Db 272 SGDIEPLIKEMVRNITDRILWLASAWATSLIAKPEYLDVVVVGTVGTFALRAGEIPGPK 331
QY 347 EFLYDVHPNKDPNDVLTIEFWQAFNCTWPNSSVPYVNDHRVNMGTGKDRLYDMSD---- 402
Db 332 DFLQEVTPKSSNEFREFWEETFNCLYLEDSE-----ORLRDSENGSTS 375
QY 403 --QLCTGEEKLELDKNVLTDSQLRITKOCKQAVYIAHGLDHLSCQEQGGPFGSNOQC 460

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Db 376 FRPLCTGEEDIMGAETPYLDYTHLRISVYVAVHSIAQALQDILTIPGRGLF-SNNSC 434
QY 461 AVIPTDFWQLMYMYKBIKFKSHEDKWIILDDNDGLKNGHYDVLNWHLD-DEGEISFTV 519
Db 435 ADIKKIEAWQLKQLRHLNFSNMGKVFHDENAD-PSGNYTIIINWHRSPEDGSWFEEV 493
QY 520 GRPNERSTNFEVLVPTNSTIFWNTESSRLPHSVCTDVCPRGTGCGFVQRPICGPDSPC 579
Db 494 GFYNMRAGKGVQLFDINTKILWNGYINTEVPFNSCEDCEPGRKGIIESMPTCCFECTEC 553
QY 580 ADGHVSRKPEGERECEQCGEDYMSNAQSECVLKEVEYLAYDEALGFTLVILSVFGAFVVL 639
Db 554 SEGEYSDHKDASVCYKCPNDWSNENHTSCFLKEIEFLSWTEPFGIALALCSVLGVFLTA 613
QY 640 AVTAVVIHRHTPLVNASDWQLGFLIQVLSLIIMLSMLFIDKPHNWSMAGQVTLALGF 699
Db 614 FVMGVFIKFRNTPIVKATNRELSYLLFLCCFSSSLIFIGEPQDWTCLRQPAFGISF 673
QY 700 SLCLSLGLKTSLSFLAYRISKSKTQLTSMHPLYRK-----IIVLSVLAIEIGICTA 751
Db 674 VLCISILVKTNRVLLVFE-AKIPTS-----LHRKWGLNLQFLVFLFTFVQVMICV 726
QY 752 YLILEPPMVYKMWESQNTKIIILGCNEISIEFLYSMEGIDAFALALLCFLTTFVARQLPDNY 811
Db 727 WLYNAPPASYNRNDIDEI-IFITCNEGSMWALGFLIGYTCLLAAICFFFPAPKSKLPENF 785
QY 812 YEGKCIITFGMLVFFIIMWSFVVPVYSTKQKFKMAVEIFAILASSHGLLGCIPAPKCLIL 871
Db 786 TEAKFITPSMLFFIIVWISFIPAYFSTYGRKFSVAVEVIAIALASSFGLLACIFENKVIIL 845
QY 872 LRPERNTSEIYCVGRVSTTDCIQLTS 897
Db 846 FKPSRNTIEEV--RCSTAASHFKVAA 869

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Job time : 171.877 secs

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